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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.45349 Seconds
(without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613b-6

Perfect score: 583

Sequence: 1 MODWLTFQKKHLNTRDVC.....TECVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	95.4	104	1	RN30_RANPI
2	292	50.1	111	1	RNP0_RANCA
3	285.5	49.0	111	1	LECS_RANCA
4	269.5	46.2	111	1	RNP1_RANCA
5	149	25.6	119	1	RNP1_IGUG
6	131	22.5	124	1	RNP_GALMU
7	130.5	22.4	145	1	ANGR_MOUSE
8	130.5	22.4	146	1	ANGI_CERAE
9	128	22.0	148	1	ANGI_BOVIN
10	126	21.6	128	1	RNP_MYOCO
11	125	21.4	124	1	RNP_BALAC
12	121.5	20.8	146	1	ANGI_MACMU
13	120	20.6	128	1	RNP_PROCU
14	119.5	20.5	145	1	ANGI_MOUSE
15	119	20.4	128	1	RNP_CAVPO
16	118.5	20.3	146	1	ANGI_PAPHA
17	117	20.1	124	1	RNP_CHIBR
18	116	19.9	125	1	ANGI_RABIT
19	116	19.9	128	1	RNP_HYDHY
20	114	19.6	144	1	ANGI_HIPAM
21	114	19.6	146	1	ANGI_MIOTA
22	113	19.4	147	1	ANGI_HUMAN
23	113	19.4	147	1	ANGI_PANTR
24	112	19.2	124	1	RNP_PIG
25	112	19.2	150	1	RNP_BOVIN
26	112	19.2	156	1	RNP_MYOGN
27	111.5	19.1	147	1	RNP_HUMAN
28	111	19.0	128	1	RNP_HORSE
29	111	19.0	128	1	RNP_HYSCR
30	111	19.0	156	1	ECP3_MOUSE
31	111	19.0	167	1	RNBR_BOVIN
32	110.5	19.0	123	1	ANGI_PIG
33	110.5	19.0	155	1	ECPI_MOUSE

34	110	18.9	141	1	RNBR_GIRCA	O29542 giraffa cam
35	110	18.9	146	1	ANGI_SACOE	O8wn62 saguinus oe
36	110	18.9	151	1	RNBR_AXIPR	P87350 axis porcine
37	109	18.7	123	1	ANG2_BOVIN	P80929 bos taurus
38	109	18.7	124	1	RNPA_CAVPO	P00678 cavia porce
39	109	18.7	124	1	RNP_AEPME	P07847 aepyretos m
40	109	18.7	124	1	RNP_ANTAM	P00668 antilocapra
41	109	18.7	124	1	RNP_SHEEP	P00661 ovis aries
42	109	18.7	146	1	ANGI_SATSC	O8wn60 salmistr sci
43	108.5	18.6	150	1	RNK6_SATSC	O46529 salmistr sci
44	108	18.5	124	1	RNP_BUBBU	P00657 bubalus bub
45	108	18.5	124	1	RNP_CONTRA	P00660 connochaete

ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	104 AA.
AC	RN30_RANPI			
AC	P22069:			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last annotation update)			
DE	P-30 protein (EC 3.1.27.-) (Onconase).			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Embryo;			
RX	MEDLINE=91093131; PubMed=1985896;			
RA	Ardelt W., Mikulski S.M., Shogen K.;			
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";			
RL	J. Biol. Chem. 266:245-251(1991).			
RN	[2]			
RP	3D-STRUCTURE MODELING.			
RX	MEDLINE=93066156; PubMed=1438177;			
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,			
RT	James M.N.G.;			
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";			
RL	Proteins 14:392-400(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RX	MEDLINE=94166079; PubMed=8120892;			
RA	Mosimann S.C., Ardelt W., James M.N.G.;			
RT	"Refined 1.7 A x-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";			
RL	J. Mol. Biol. 236:1141-1153(1994).			
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPILOLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO. AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.			
CC	-1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PDB: 1ONC; 31-JAN-94.			
DR	InterPro: IPR001427; RnaseA.			
DR	Pfam: PF00074; RnaseA; 1.			
DR	Prodom: PD000535; RnaseA; 1.			
DR	SMART: SM00092; RnaseA; 1.			
DR	PROSITE: PS00127; RnaseA; 1.			
KW	Hydrolyase; Nuclease; Endonuclease; 3D-structure.			
FT	MOD_RSS 1			
FT	ACT_SITE 10			
FT	ACT_SITE 31			
FT	ACT_SITE 97			
FT	DISULFID 19			
FT	DISULFID 30			
FT	DISULFID 48			
FT	DISULFID 90			

FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT TURN 23 24
 FT TURN 26 30
 FT STRAND 33 38
 FT HELIX 41 48
 FT TURN 49 50
 FT STRAND 55 58
 FT TURN 63 70
 FT TURN 74 75
 FT STRAND 77 84
 FT STRAND 86 91
 FT TURN 92 93
 FT STRAND 94 101
 SO SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 95.4%; Score 556; DB 1; Length 104;
 Best Local Similarity 96.2%; Pred. No. 1,3e-52;
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAICGIIASKNVLT 61
 DB 1 QDWLTFQKHLTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAICGIIASKNVLT 60
 QY 62 SEFYLSDCNVTSPCKYKLLKSTNTECVTCENQAPVHFVGVGHC 105
 DB 61 SEFYLSDCNVTSPCKYKLLKSTNTECVTCENQAPVHFVGVGSC 104

RESULT 2
 RNPO_RANCA STANDARD; PRT; 111 AA.
 ID RNPO_RANCA STANDARD; PRT; 111 AA.

DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
 DE Rana catesbeiana (Bull. frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN 11
 RP SEQUENCE.
 RC TISSUE-Egg;
 RX MEDLINE=67299649; PubMed=3304421;
 RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
 RA Takayanagi G., Hakomori S.;
 RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
 catesbeiana) eggs.";
 RL Biochemistry 26:2189-2194(1987).
 RN 12
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
 RX MEDLINE=92220613; PubMed=137337;
 RA Liao Y.-D.;
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
 catesbeiana (bullfrog) oocytes.";
 RL Nucleic Acids Res. 20:1371-1377(1992).
 RN 13
 RP CHARACTERIZATION.
 RC TISSUE-Egg;
 RX MEDLINE=93192604; PubMed=8448385;
 RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
 RA Takayanagi Y., Hakomori S., Titani K.;
 RT "Ribonuclease activity of sialic acid-binding lectin from Rana
 catesbeiana eggs.";
 RL Glycobiology 3:37-45(1993).
 RN 14
 RP STRUCTURE BY NMR.
 RX MEDLINE=98437383; PubMed=9761686;
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

RT "The solution structure of a cytotoxic ribonuclease from the oocytes
 of Rana catesbeiana (bullfrog).";
 RL J. Mol. Biol. 283:231-244(1998).
 CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
 RESIDUES WITH A 3' FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)
 AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS
 MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG
 EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING
 NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND
 HUMAN ORIGIN.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A27121; A27121.
 DR PDB: 1BC4; 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_PC; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; lectin; 3D-structure.
 FT MOD_RES 1 1
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SO SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECF4 CRC64;

Query Match 50.1%; Score 292; DB 1; Length 111;
 Best Local Similarity 49.5%; Pred. No. 1.8e-24;
 Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 2 QDWLTFQKHLTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAICGIIASKN 57
 DB 1 QDWLTFQKHLTNRDVDCNNIMSTNLFHCKDKNTFTYSRPEPYKAICGIIASKN 59
 QY 58 VLTSEFYLSDC---NTSPCKYKLLKSTNTECVTCENQAPVHFVGVGHC 105
 DB 60 VLTSEFYLSDC---NTSPCKYKLLKSTNTECVTCENQAPVHFVGVGHC 110

RESULT 3
 LECS_RANJA STANDARD; PRT; 111 AA.
 ID LECS_RANJA STANDARD; PRT; 111 AA.
 AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sialic acid-binding lectin (EC 3.1.27.-).
 DE Rana japonica (Japanese reddish frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN 11
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE-Egg;
 RX MEDLINE=91035319; PubMed=2229005;
 RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
 RA Takayanagi Y., Titani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
 eggs.";
 RL J. Biochem. 108:139-143(1990).
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
 FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
 PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
 DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0120; JX0120.

DR HSSP; P11916; IBC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNaseA: 1.
 DR PROSITE: PS00127; RNaseA: PANCREATIC; 1.
 DR HydroLase: Nuclease: Endonuclease; Sialic acid; Lectin.
 FT MOD_RES 1
 FT ACT_SITE 10
 FT ACT_SITE 35
 FT ACT_SITE 103
 FT ACT_SITE 103
 FT DISULFID 19
 FT DISULFID 34
 FT DISULFID 52
 FT DISULFID 94
 FT DISULFID 111
 SO SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 49.08; Score 285.5; DB 1; Length 111;
 Best Local Similarity 45.08; Pred. No. 9.1e-24;
 Matches 50; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

OY 2 QDWLTFOKHLNTRDYDCNNIMSTNLF---HCKDKNTFYSPREPVAICGIIASKN 57
 1 QNMAKFEKHIPTNSNTNNTIMDKSIYVGCKEKERTFTISSATTVKAICSGASTNRN 60
 DB 58 VLTTFSEYLSDC---NVTSPCKYKLLKSTNFTCVTCENAPVHFVGVGHC 105
 61 VLTSTFRQNTCTIRSATAPRCPYNSRTETNVICVCKENRLPVHFAIGRC 111

RESULT 4

RNPL_RANCA STANDARD; PRT; 111 AA.
 ID RNPL_RANCA
 AC P14626;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, liver (EC 3.1.27.5).
 OS Rana catesbeiana (Bull frog).
 CC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Eukaryota; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90130374; Pubmed=2613682;
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
 RT liver.";
 FT J. Biochem. 106:729-735(1989).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR HSSP; P11916; IBC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNaseA: 1.
 DR PROSITE: PS00127; RNaseA: PANCREATIC; 1.
 DR HydroLase: Nuclease: Endonuclease.
 FT MOD_RES 1
 FT ACT_SITE 10
 FT ACT_SITE 35
 FT ACT_SITE 104
 FT ACT_SITE 104
 FT DISULFID 19
 FT DISULFID 34
 FT DISULFID 52
 FT DISULFID 94
 FT DISULFID 111
 SO SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 46.28; Score 269.5; DB 1; Length 111;
 Best Local Similarity 43.28; Pred. No. 4.6e-22;
 Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

OY 2 QDWLTFOKHLNTRDYDCNNIMSTNLF---HCKDKNTFYSPREPVAICGIIASKN 57
 1 QNMAKFEKHIPTNSNTNNTIMDKSIYVGCKEKERTFTISSATTVKAICSGASTNRN 60
 DB 58 VLTTFSEYLSDC---NVTSPCKYKLLKSTNFTCVTCENAPVHFVGVGHC 105
 61 VLTSTFRQNTCTIRSATAPRCPYNSRTETNVICVCKENRLPVHFAIGRC 111

RESULT 5

RNP_IGUG STANDARD; PRT; 119 AA.
 ID RNP_IGUG
 AC P80287;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 OS Iguana iguana (Common Iguana).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
 OX NCBI_TaxID=8517;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=94139745; Pubmed=8307028;
 RA Zhao W., Beintema J.J., Hofsteenge J.;
 RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic
 RT ribonuclease.";
 FT Eur. J. Biochem. 219:641-646(1994).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR HSSP; P00656; ILSQ.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR PRINTS: PRO0794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNaseA: 1.
 DR PROSITE: PS00127; RNaseA: PANCREATIC; 1.
 DR HydroLase: Nuclease: Endonuclease.
 FT MOD_RES 1
 FT DISULFID 25
 FT DISULFID 39
 FT DISULFID 57
 FT DISULFID 106
 FT ACT_SITE 10
 FT ACT_SITE 40
 FT ACT_SITE 113
 FT ACT_SITE 113
 SO SEQUENCE 119 AA; 13324 MW; 6072FEB5B7B15BD5A CRC64;

Query Match 25.68; Score 149; DB 1; Length 119;
 Best Local Similarity 30.78; Pred. No. 3.4e-09;
 Matches 35; Conservative 19; Mismatches 44; Indels 16; Gaps 5;

OY 2 QDWLTFOKHLNTRDYDCNNIMSTNLFCKDKNTFYSPREPVAIC--K.50
 1 QNMAKFEKHIPTNSNTNNTIMDKSIYVGCKEKERTFTISSATTVKAICSGASTNRN 60
 DB 51 GIASKNVLTSE-FYLSDC---NVTSPCKYKLLKSTNFTCVTCENAPVHF 99
 61 GTHYEDNLVDNSESFDLTDCKNVGCTAPSSCKYNGCTGTRIRIACENQPVHF 114

RESULT 6
 RNP_GALMU STANDARD; PRT; 124 AA.
 ID RNP_GALMU

AC P00680;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 GN RNASE1 OR RNS1.
 OS Galea musteloides (Cul's).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriognath; Cavidae; Galea.
 OX NCBI_TaxID=10146;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87036770; PubMed=6571219;
 RA "Bentema J.J., Neuteboom B.;
 RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
 RT of the amino acid sequences with those of two close relatives:
 RT capybara and cul's ribonuclease";
 RL J. Mol. Evol. 19:145-152(1983).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00827; NR01.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RnaseA.
 DR Pfam: PF00074; rnasea; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RnaseA; 1.
 DR SMART: SM00092; Rnase_Pc; 1.
 DR PROSITE: PS00127; Rnase_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 65 112 BY SIMILARITY.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
 SQ SEQUENCE 124 AA: 13870 MW: 60937E251A7BBA25 CXC64;
 Query Match 22.5%; Score 131; DB 1; Length 124;
 Best Local Similarity 30.6%; Pred. No. 3e-07;
 Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;
 OY 5 LTPQKHL-----TNRDVCNNIM---STNLFHCCKDTFTYSRPEPKAICKGIIA 54
 DB 6 MKFQRHMDSDGHPDTNTN--YCNEMVRRSMTOGRCKPVTFFVHEPLEAVQAVC----S 59
 OY 55 SKNV-----LTTSEFYLSDCNVTSRP-----CKYELKSKTNTFCVTGEN--QAPVH 98
 DB 60 QKNVPCKKNGQTCNQSHSMRTITDORVITSSSKYPCSTRMTOAKSITIVACEGIPSVVPH 119
 OY 99 F 99
 DB 120 F 120
 RESULT 7
 ANGR_MOUSE STANDARD: PRT; 145 AA.
 AC Q64438;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Angiogenin-related protein precursor.
 GN ANGRP.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Liver;
 RX MEDLINE=96079109; PubMed=8530072;
 RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
 RT "The mouse angiogenin gene family: structures of an angiogenin-related
 RT protein gene and two pseudogenes";
 RL Genomics 29:200-206(1995).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U22519; AAA91367.1; -;
 DR HSSP: P03950; IAAV.
 DR MGD: MGI:104984; Angrp.
 DR InterPro: IPR001427; RnaseA.
 DR Pfam: PF00074; rnasea; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RnaseA; 1.
 DR SMART: SM00092; Rnase_Pc; 1.
 DR PROSITE: PS00127; Rnase_PANCREATIC; 1.
 KW Signal; Hydrolyase; Nuclease; Endonuclease.
 FT SIGNAL 1 24
 FT CHAIN 25 145 ANGIOGENIN-RELATED PROTEIN.
 FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).
 FT ACT_SITE 37 37 BY SIMILARITY.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 137 137 BY SIMILARITY.
 FT DISULFID 50 104 BY SIMILARITY.
 FT DISULFID 63 115 BY SIMILARITY.
 FT DISULFID 81 130 BY SIMILARITY.
 SQ SEQUENCE 145 AA: 16612 MW: 2946EB814429C4AD CXC64;
 Query Match 22.4%; Score 130.5; DB 1; Length 145;
 Best Local Similarity 38.2%; Pred. No. 4e-07;
 Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;
 OY 31 CKDKNTFTYSRPEPKAIC--KGIIASKNV--LTTSEFYLSDCNVTSR-----PCYKYLKKS 83
 DB 63 CKDVNTFTIHDTRKNNIKATCGKKGSPYGRNLKISRSFOVYCTHKGRSPRPCKTRASKG 122
 OY 84 TTFECVTCENQAPVHF 99
 DB 123 FRYIIIGCENGMPVHF 138
 RESULT 8
 ANGI_CERAE STANDARD: PRT; 146 AA.
 AC Q8WN66;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).
 GN ANG OR RNASE5.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21918422; PubMed=11919285;
 RA Zhang J., Rosenberg H.F.;
 RT "Diversifying selection of the tumor-growth promoter angiogenin in
 RT primate evolution.";

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RL Mol. Biol. Evol. 19:438-445(2002).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/).
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF441664; AAL61646.1; -
KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
KM Protein synthesis inhibitor; Signal
FT SIGNAL 1 24
FT CHAIN 25 146
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 138 138
FT DISULFID 50 105
FT DISULFID 63 116
FT DISULFID 81 131
SQ SEQUENCE 146 AA; 16444 MW; 27860112E858DF9 CRC64;

Query March 22.4%; Score 130.5; DB 1; Length 146;
Best Local Similarity 30.7%; Pred. No. 4e-07; Mismatches 30; Indels 23; Gaps 4;
Matches 31; Conservativity 17;

OY 6 TFQKHLNLTFRDVCNNIMSTNLFCKDKNTFTYSRPEVKAIC--KGIIASKNV-LTT 61
Db 53 TMRRRHLLTSP-----CKDINFTIGNRHRIKALICGDEGNPNYGENLRISK 97
OY 62 SEFYLDSCNVTST---RCKYKLLKSTNPTCVGCENQARVN 98
Db 98 SPFOVYTCNLKRGSGSPRRCQYRATRGSRNIVYVGCENGLPVH 138

RESULT 9
AC ANGI_BOVIN STANDARD; PRT; 148 AA.
ID ANGI_BOVIN
AC P10152; O9GKP9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
GN Angiogenin-1 precursor (EC 3.1.27.-).
GN ANGI OR ANG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Layer;
RA Chang S.-I.;
RA "Cloning, sequencing, and expression of bovine angiogenin.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN 12
RC SEQUENCE OF 24-148.
RX MEDLINE=86065101; PubMed=3197838;
RX Maes P., Damsart D., Kommens C., Montreuil J., Spik G., Tartar A.;
RX "The complete amino acid sequence of bovine milk angiogenin.";

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RN FEBS Lett. 241:41-45(1988).
 RL [3] SEQUENCE OF 24-148.
 RP TISSUE=Plasma;
 RC MEDLINE=89375344; PubMed=2775757;
 RA Bond M.D., Strydom D.J.;
 RL "Amino acid sequence of bovine angiogenin."; Biochemistry 28:6110-6113(1989).
 RN [4]
 RP CHARACTERIZATION, AND SEQUENCE OF 25-55.
 RC TISSUE=Plasma;
 RX MEDLINE=69118214; PubMed=3064806;
 RA Bond M.D., Vallee B.L.;
 RL "Isolation of bovine angiogenin using a placental ribonuclease inhibitor binding assay."; Biochemistry 27:6282-6287(1988).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE=95224057; PubMed=7708754;
 RA Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
 RL "Crystal structure of bovine angiogenin at 1.5-A resolution."; Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=96280645; PubMed=8688423;
 RA Leguin O., Albarret C., Bonlems F., Spik G., Lallemand J.-Y.;
 RL "Solution structure of bovine angiogenin by IH nuclear magnetic resonance spectroscopy."; Biochemistry 35:8870-8880(1996).
 CC -I- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAs. BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- TISSUE SPECIFICITY: SERUM, AND MILK.
 CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF135124; AAG47631.1; -
 DR PIR; A32474; A32474.
 DR PDB; 1AGI; 03-APR-96.
 DR PDB; 1G10; 07-DEC-96.
 DR InterPro: IPR001427; RnaseA.
 DR Pfam; PF00074; RnaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR PRODOM; PD000535; RnaseA; 1.
 DR SMART; SM00092; Rnase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Angiogenesis; Protein synthesis inhibitor; Signal; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 148 ANGIOENIN-1.
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 138 138
 FT DISULFID 50 105
 FT DISULFID 63 116
 FT DISULFID 81 131
 SQ SEQUENCE 148 AA; 16969 MW; B7999124CBB523DD CRC64;
 Query Match 22.0%; Score 128; DB 1; Length 148;
 Best Local Similarity 34.0%; Pred. NO. 7.5e-07;

Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

QY 17 DVDCNNINSLNF--HCKDKNTFYTSRPEPVKAICKGIASKN-----VLTTSEFL 66
 Db 47 DEYCFNMKNRRLTRPCCKDRNTFHKMKNDKALCE-----DRNQPIRGDLRISKSEFOI 102

QY 67 SDC---NVTSR-PEKYALKSTNTFCVTCENQAPVHF 99
 Db 103 TICKHGSGSRPPCRGATEDSRVIVGCEGCLPVHF 139

RESULT 10
 RNP_MYOCO
 ID RNP_MYOCO STANDARD; PRT; 128 AA.

AC P00676; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 GN RNASEL OR RNSL.
 OS Myocastor coypus (Coypu) (Nutria).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;
 CC Myocastor.
 CC NCBI_TaxID=10157;
 RN (1)

RP SEQUENCE.
 RC TISSUE-Pancreas;
 RA MEDLINE=7065676; Pubmed=999896;
 RX van den Berg A., van den Hende-Timmer L., Beintema J.J.;
 RT "Isolation, properties and primary structure of coypu and chinchilla
 pancreatic ribonuclease.";
 RL Biochem. Biophys. Acta 453:400-409(1976).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00822; NRCU.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 DR KMW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT ACT_SITE 65 72 BY SIMILARITY.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .);
 SQ SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

Query Match 21.6%; Score 126; DB 1; Length 128;
 Best Local Similarity 29.9%; Pred. No. 1e-06;
 Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 7 FQKHL-----TNRDVCNNIM-STNLF--HCKDKNTFYTSRPEPVKAICKGIASKN 58
 Db 8 FERQHMDSRGSPSTNPVNCNEMKSRMTOGRCKPVTVEFHEPLADQAVC-----FQKNV 63

QY 59 L-----TTFEFLSDCQNTVSRP---CYKALKSTNTFCVTCENQ--APVHF 99
 Db 64 LCKNGQTCYQSNMHTDCRVTNSDYPNCSYRTSQEKSIVVACEGPNYVPVHF 120

RESULT 11
 RNP_BALAC
 ID RNP_BALAC STANDARD; PRT; 124 AA.

AC P00673; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 GN RNASEL OR RNSL.
 OS Balaenoptera acutirostrata (Mink whale) (lesser rorqual).
 CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 CC Balaenopteridae; Balaenoptera.
 CC NCBI_TaxID=9767;
 RN (1)

RP SEQUENCE.
 RC MEDLINE=76277855; Pubmed=962870;
 RX Emmons M., Welling G.W., Beintema J.J.;
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
 ribonuclease.";
 RL Biochem. J. 157:317-323(1976).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00818; NRMK.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 DR KMW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT ACT_SITE 65 72 BY SIMILARITY.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .); IN 30% OF THE
 MOLECULES.
 SQ SEQUENCE 124 AA; 14125 MW; F57475459697E20 CRC64;

Query Match 21.4%; Score 125; DB 1; Length 124;
 Best Local Similarity 28.6%; Pred. No. 1.3e-06;
 Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

QY 5 LTFQKHLTNRDVCNNIMSTNLF--HCKDKNTFYTSRPEPVKAICKGIASKN 56
 Db 6 MKFORQHMDSGNSPNNPNPCNQMRRKMTQGRCKPVTVEFHESELEKAVNC-----SQK 61

QY 57 NVL-----TTFEFLSDCQNTVSRP---CYKALKSTNTFCVTCENQ--APVHF 99
 Db 62 NVLCKNGRTNCYESNHTDRCQTCROTQSSKYPNCAKYTSQREKHLIVACGPNYVPVHF 120

RESULT 12
 ANGI_MACMU
 ID ANGI_MACMU STANDARD; PRT; 146 AA.

AC Q8W63; 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).
 GN ANG OR RNASE5.
 OS Macaca mulatta (Rhesus macaque).
 CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 CC NCBI_TaxID=9544;
 RN (1)

CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U22516; AAA91366.1; -
DR PIR: A35932; A35932.
DR HSSP: P03950; 1A4Y.
DR MGD: MGI:88022; Ang.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
KM Protein synthesis inhibitor; Signal.
FT CHAIN 1 24
FT MOD_RES 25 25 ANGIOGENIN.
FT ACT_SITE 37 37 PYRROLIDONE CARBOXYLIC ACID (BY
FT ACT_SITE 64 64 SIMILARITY).
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16228 MW; 06944260B8764938 CRC64;
Query Match 20.5%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 5.9e-06;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;
QY 10 KHLNTRDND-----CNINSTNLF--HCKDKNTFIYSRPEPKAIC--KGIASKN 57
Db 32 KFLTQNHDAKRGDRDRCERMKRSLSPCKDVTMFHGNKSNKAIKGANGSPYREN 91
QY 58 V-LITSEFYLSDCNVTN----RPCKYKLLKSTNTFCVTCENQAPVHF 99
Db 92 LRMSKSPFOYTCKHTGSGSPRPOCYRASAGFRHVIACENGLPVHF 138
RESULT 15
RNPB_CAVPO STANDARD; PRT; 128 AA.
ID RNPB_CAVPO
AC P00679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=77185023; PubMed=862624;
RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastera W.,
RA Beintema J.J.;
RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT structure and glycosylation."
RT Eur. J. Biochem. 75:91-100(1977).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC PIR: A00826; NRGPB.
DR HSSP: P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT VARIANT 64 64 L -> P.
SQ SEQUENCE 128 AA; 14406 MW; A2FA101A1A3393B CRC64;
Query Match 20.4%; Score 119; DB 1; Length 128;
Best Local Similarity 28.3%; Pred. No. 5.8e-06;
Matches 34; Conservative 21; Mismatches 35; Indels 30; Gaps 7;
QY 5 LTFQKKHL-----TNRDVCNNIM--STNLFHCKDKNTFIYSRPEPKAICKGIAS 55
Db 6 MKQROHMDGSPSSNSN--CNVMMIRNMTGGRCKPNTFVHESLADYQAVC-----PQ 60
QY 56 KNLV-----TTSEFYLSDCNVTSRP---CKYKLLKSTNTFCVTCENQ--APVHF 99
Db 61 KNLCKNKGQTCNVCYSRMRITDCAVTTSSSKFPNCYSRMSQAQKSIIVACEGDPVYVHF 120
Search completed: June 25, 2003, 14:50:03
Job time : 6.45349 secs